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Biotechnology Systems Branch

FAX TRANSMISSION COVER SHEET

DATE: _04/26/2006_   Total Number of Pages Faxed: _8_

TO:

NAME: _Thomson James_

ORG.: _____

FAX NUMBER: _571 - 273 - 0459_

FROM: Mark Spencer
Voice Ph. Number: (571)272-2510
FAX Ph. Number: (571)273-0221 ✓
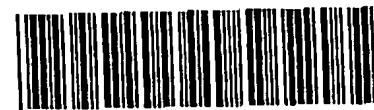
Message:

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____10/516, 075_____

Source: _____PCT_____

Date Processed by STIC: _____04/26/2006_____

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RAW SEQUENCE LISTING   DATE: 04/26/2006
PATENT APPLICATION: US/10/516,075   TIME: 09:48:11

Input Set : E:\Final Sequence list 13173-00012-US.txt
Output Set: N:\CRF4\04262006\J516075.raw

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 3 <110> APPLICANT: Sonnewald, Uwe
 4        Bornke, Frederik
 5        Herbers, Karin
 6        Tschiersch, Bettina
 7        Neuhaus, Horst-Ekkehard
 9 <120> TITLE OF INVENTION: Methods for obtaining pathogen resistance in plants
11 <130> FILE REFERENCE: 13173-00012-US
13 <140> CURRENT APPLICATION NUMBER: US 10/516,075
14 <141> CURRENT FILING DATE: 2004-11-29
16 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/007027
17 <151> PRIOR FILING DATE: 2003-07-02
19 <150> PRIOR APPLICATION NUMBER: DE 102 30 220.0
20 <151> PRIOR FILING DATE: 2002-07-04
22 <160> NUMBER OF SEQ ID NOS: 36
24 <170> SOFTWARE: PatentIn version 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1890
29 <212> TYPE: DNA
30 <213> ORGANISM: Protaminobacter rubrum
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1887)
35 <223> OTHER INFORMATION: coding for sucrose isomerase
37 <400> SEQUENCE: 1
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40  1               5                  10                  15
41 tca tta tgc atc tca tgc cag caa gcc ttc ggt acg caa caa ccc ttg   96
42 Ser Leu Cys Ile Ser Cys Gln Gln Ala Phe Gly Thr Gln Gln Pro Leu
43                20                  25                  30
44 ctt aac gaa aag agt atc gaa cag tcg aaa acc ata cct aaa tgg tgg  144
45 Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp
46                35                  40                  45
47 aag gag gct gtt ttt tat cag gtg tat ccg cgc tcc ttt aaa gac acc  192
48 Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
49        50                  55                  60
50 aac gga gat ggc atc ggg gat att aac ggc atc ata gaa aaa tta gac  240
51 Asn Gly Asp Gly Ile Gly Asp Ile Asn Gly Ile Ile Glu Lys Leu Asp
52  65                  70                  75                  80
53 tat cta aaa gcc ttg ggg att gat gcc att tgg atc aac cca cat tat  288
54 Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
55                85                  90                  95
56 gat tct ccg aac acg gat aat ggt tac gat ata cgt gat tat cga aaa  336
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Input Set : E:\Final Sequence list-13173-00012-US.txt
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57 Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
58              100                 105                 110
59 atc atg aaa gaa tat ggc acg atg gag gat ttt gac cgc ctg att tct    384
60 Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
61          115                 120                 125
62 gaa atg aaa aaa cgg aat atg cgg ttg atg att gat gtg gtc atc aac    432
63 Glu Met Lys Lys Arg Asn Met Pro Leu Met Ile Asp Val Val Ile Asn
64          130                 135                 140
65 cac acc agc gat caa aac gaa tgg ttt gtt aaa agt aaa agc agt aag    480
66 His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys
67 145                 150                 155                 160
68 gat aat cct tat cgc ggc tat tat ttc tgg aaa gat gct aaa gaa ggg    528
69 Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly
70              165                 170                 175
71 cag gcg cct aat aat tac cct tca ttc ttt ggt ggc tcg gcg tgg caa    576
72 Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
73              180                 185                 190
74 aaa gat gaa aag acc aat caa tac tac ctg cac tat ttt gct aaa caa    624
75 Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
76              195                 200                 205
77 cag cct gac cta aac tgg gat aat ccc aaa gtc cgt caa gat ctt tat    672
78 Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
79          210                 215                 220
80 gca atg tta cgt ttc tgg tta gat aaa ggc gtg tct ggt tta cgt ttt    720
81 Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
82 225                 230                 235                 240
83 gat acg gta gcg acc tac tca aaa att ccg gat ttc cca aat ctc acc    768
84 Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr
85              245                 250                 255
86 caa caa cag ctg aag aat ttt gca gcg gag tat acc aag ggc cct aat    816
87 Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn
88          260                 265                 270
89 att cat cgt tac gtc aat gaa atg aat aaa gag gtc ttg tct cat tac    864
90 Ile His Arg Tyr Val Asn Glu Met Asn Lys Glu Val Leu Ser His Tyr
91          275                 280                 285
92 gac att gcg act gcc ggt gaa atc ttt ggc gta ccc ttg gat caa tcg    912
93 Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser
94          290                 295                 300
95 ata aag ttc ttc gat cgc cgc cgt gat gag ctg aac att gca ttt acc    960
96 Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr
97 305                 310                 315                 320
98 ttt gac tta atc aga ctc gat cga gac tct gat caa aga tgg cgt cga   1008
99 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg
100              325                 330                 335
101 aaa gat tgg aaa ttg tcg caa ttc cgg cag atc atc gat aac gtt gac   1056
102 Lys Asp Trp Lys Leu Ser Gln Phe Arg Gln Ile Ile Asp Asn Val Asp
103              340                 345                 350
104 cgt act gca gga gaa tat ggt tgg aat gcc ttc ttc ttg gat aac cac   1104
105 Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
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106         355                 360                 365
107 gac aat ccg cgc gct gtc tcg cac ttt ggc gat gat gat cgc cca caa   1152
108 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Asp Arg Pro Gln
109         370                 375                 380
110 tgg cgt gag cca tcg gct aaa gcg ctt gca acc ttg acg ctg act caa   1200
111 Trp Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln
112 385                 390                 395                 400
113 cga gca aca cct ttt att tat caa ggt tca gaa ttg ggc atg acc aat   1248
114 Arg Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn
115                     405                 410                 415
116 tac ccg ttt aaa gct att gat gaa ttc gat gat att gag gtg aaa ggt   1296
117 Tyr Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly
118                 420                 425                 430
119 ttt tgg cat gac tac gtt gag aca gga aag gtc aaa gcc gac gag ttc   1344
120 Phe Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe
121                 435                 440                 445
122 ttg caa aat gta cgc ctg acg agc agg gat aac agc cgg acg ccg ttc   1392
123 Leu Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe
124         450                 455                 460
125 caa tgg gac ggg agc aaa gac gca gga ttc acg agc gga aaa cct tgg   1440
126 Gln Trp Asp Gly Ser Lys Asp Ala Gly Phe Thr Ser Gly Lys Pro Trp
127 465                 470                 475                 480
128 ttc aag gtc aac cca aac tac cag gaa atc aat gca gta agt caa gtc   1488
129 Phe Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val
130                     485                 490                 495
131 aca caa ccc gac tca gta ttt aac tat tat cgt cag ttg atc aag ata   1536
132 Thr Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile
133                 500                 505                 510
134 agg cat gac atc ccg gca ctg acc tat ggt aca tac acc gat ttg gat   1584
135 Arg His Asp Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp
136         515                 520                 525
137 cct gca aat gat tcg gtc tac gcc tat aca cgc agc ctt ggg gcg gaa   1632
138 Pro Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu
139         530                 535                 540
140 aaa tat ctt gtt gtt gtt aac ttc aag gag caa atg atg aga tat aaa   1680
141 Lys Tyr Leu Val Val Val Asn Phe Lys Glu Gln Met Met Arg Tyr Lys
142 545                 550                 555                 560
143 tta ccg gat aat tta tcc att gag aaa gtg att ata gac agc aac agc   1728
144 Leu Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Asp Ser Asn Ser
145                     565                 570                 575
146 aaa aac gtg gtg aaa aag aat gat tca tta ctc gag cta aaa cca tgg   1776
147 Lys Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp
148                 580                 585                 590
149 cag tca ggg gtt tat aaa act aaa tca ata aat ctc ata gtc acg cca   1824
150 Gln Ser Gly Val Tyr Lys Thr Lys Ser Ile Asn Leu Ile Val Thr Pro
151         595                 600                 605
152 aat aat gta aat ata ttg aaa cta tta aaa ccg gca ttt tat gcc ggt   1872
153 Asn Asn Val Asn Ile Leu Lys Leu Leu Lys Pro Ala Phe Tyr Ala Gly
154         610                 615                 620
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/516,075

DATE: 04/26/2006
TIME: 09:48:11

Input Set : E:\Final Sequence list-13173-00012-US.txt
Output Set: N:\CRF4\04262006\J516075.raw

1890

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155 ttt ttt agc gca aaa tag
156 Phe Phe Ser Ala Lys
157 625
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 629
162 <212> TYPE: PRT
163 <213> ORGANISM: Protaminobacter rubrum
165 <400> SEQUENCE: 2
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167   1               5                  10                  15
168 Ser Leu Cys Ile Ser Cys Gln Gln Ala Phe Gly Thr Gln Gln Pro Leu
169              20                  25                  30
170 Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp
171              35                  40                  45
172 Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
173              50                  55                  60
174 Asn Gly Asp Gly Ile Gly Asp Ile Asn Gly Ile Ile Glu Lys Leu Asp
175   65                  70                  75                  80
176 Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
177                  85                  90                  95
178 Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
179              100                 105                 110
180 Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
181             115                 120                 125
182 Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
183         130                 135                 140
184 His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys
185 145                 150                 155                 160
186 Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly
187                 165                 170                 175
188 Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
189             180                 185                 190
190 Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
191             195                 200                 205
192 Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
193         210                 215                 220
194 Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
195 225                 230                 235                 240
196 Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr
197             245                 250                 255
198 Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn
199             260                 265                 270
200 Ile His Arg Tyr Val Asn Glu Met Asn Lys Glu Val Leu Ser His Tyr
201             275                 280                 285
202 Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser
203         290                 295                 300
204 Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr
205 305                 310                 315                 320
206 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg
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207                   325              330              335
208 Lys Asp Trp Lys Leu Ser Gln Phe Arg Gln Ile Ile Asp Asn Val Asp
209               340              345              350
210 Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
211           355              360              365
212 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Asp Arg Pro Gln
213       370              375              380
214 Trp Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln
215 385          390              395                  400
216 Arg Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn
217               405              410              415
218 Tyr Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly
219           420              425              430
220 Phe Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe
221           435              440              445
222 Leu Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe
223       450              455              460
224 Gln Trp Asp Gly Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp
225 465              470              475                  480
226 Phe Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val
227               485              490              495
228 Thr Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile
229           500              505              510
230 Arg His Asp Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp
231           515              520              525
232 Pro Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu
233       530              535              540
234 Lys Tyr Leu Val Val Val Asn Phe Lys Glu Gln Met Met Arg Tyr Lys
235 545              550              555                  560
236 Leu Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Asp Ser Asn Ser
237               565              570              575
238 Lys Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp
239           580              585              590
240 Gln Ser Gly Val Tyr Lys Thr Lys Ser Ile Asn Leu Ile Val Thr Pro
241           595              600              605
242 Asn Asn Val Asn Ile Leu Lys Leu Leu Lys Pro Ala Phe Tyr Ala Gly
243       610              615              620
244 Phe Phe Ser Ala Lys
245 625
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 1305
250 <212> TYPE: DNA
251 <213> ORGANISM: Erwinia rhapontici
254 <220> FEATURE:
255 <221> NAME/KEY: CDS
256 <222> LOCATION: (1)..(1305)
257 <223> OTHER INFORMATION: coding for N-terminal fragment of sucrose isomerase
259 <220> FEATURE:
260 <221> NAME/KEY: misc_feature
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/26/2006
PATENT APPLICATION: US/10/516,075   TIME: 09:48:12

Input Set : E:\Final Sequence list-13173-00012-US.txt
Output Set: N:\CRF4\04262006\J516075.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 28,85,86,87
Seq#:3; Xaa Pos. 10,29
Seq#:4; Xaa Pos. 10,29
Seq#:9; Xaa Pos. 270,491
Seq#:10; Xaa Pos. 270,491
Seq#:21; N Pos. 1237,1238,1239,1240,1241,1242,1243,1244,1245,1246,1247,1248
Seq#:21; N Pos. 1249,1250,1251,1252,1253,1254,1255,1256,1257,1258,1259,1260
Seq#:21; N Pos. 1261,1262,1263,1264,1265,1266,1267,1268,1269,1270,1271,1272
Seq#:21; N Pos. 1273,1274,1275,1276,1277,1278,1279,1280,1281,1282,1283,1284
Seq#:21; N Pos. 1285,1286,1287,1288,1289,1290,1291,1292,1293,1294,1295,1296
Seq#:21; N Pos. 1297,1298,1299,1300,1301,1302,1303,1304,1305,1306,1307,1308
Seq#:21; N Pos. 1309,1310,1311,1312,1313,1314,1315,1316,1317,1318,1319,1320
Seq#:21; N Pos. 1321,1322,1323,1324,1325,1326,1327,1328,1329,1330,1331
Seq#:21; Xaa Pos. 413,414,415,416,417,418,419,420,421,422,423,424,425,426
Seq#:21; Xaa Pos. 427,428,429,430,431,432,433,434,435,436,437,438,439,440
Seq#:21; Xaa Pos. 441,442,443,444
Seq#:22; Xaa Pos. 413,414,415,416,417,418,419,420,421,422,423,424,425,426
Seq#:22; Xaa Pos. 427,428,429,430,431,432,433,434,435,436,437,438,439,440
Seq#:22; Xaa Pos. 441,442,443,444

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/516,075

DATE: 04/26/2006
TIME: 09:48:12

Input Set : E:\Final Sequence list-13173-00012-US.txt
Output Set: N:\CRF4\04262006\J516075.raw

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:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:48
:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:48
:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:96
:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16
:914 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:816
L:956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1488
L:1030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:256
L:1058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:480
L:2120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:1200
L:2121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:1248
L:2123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:1248
L:2124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:1296
L:2126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:1296
L:2127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:1344
L:2229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:400
L:2231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:416
L:2233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:432
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file: //C:\CRF4\Outhold\VsrJ516075.htm